

18 NOV 2005

SEQUENCE LISTING

<110> BIOGEN, INC.

<120> THERAPIES FOR RENAL FAILURE USING INTERFERON-BETA

<130> BII-001.25

<140> PCT/US03/22440

<141> 2003-07-17

<150> US 60/396,393

<151> 2002-07-17

<160> 21

<170> PatentIn Ver. 2.1

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<211> 840

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (76)..(636)

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Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu  
1 5 10

ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159  
Leu Cys Phe Ser Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly  
15 20 25

tgc cta caa aga agc aat ttt cag tgt cag aag ctc ctg tgg caa 207  
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln  
30 35 40

ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255  
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp  
45 50 55 60

atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303  
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala  
65 70 75

gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351  
Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg  
80 85 90

caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399  
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu  
95 100 105

ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447  
 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu  
   110                   115                   120  
  
 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt 495  
 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser  
   125                   130                   135                   140  
  
 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc 543  
 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala  
   145                   150                   155  
  
 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta 591  
 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu  
   160                   165                   170  
  
 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac 636  
 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
   175                   180                   185  
  
 tgaagatctc ctagcctgtg cctctggac tggacaattt cttcaaggcat tcttcaacca 696  
 gcagatgctg tttaagtgac tgatggctaa tgtactgcat atgaaaggac actagaagat 756  
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 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg  
   20                25                30  
  
 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg  
   35                40                45  
  
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu  
   50                55                60  
  
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile  
   65                70                75                80  
  
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser  
   85                90                95  
  
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
   100               105               110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu  
115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys  
130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser  
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His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr  
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
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<222> (1)..(498)

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1 5 10 15

tgt cag aag ctc ctg tgg caa ttg aat ggg agg ctt gaa tac tgc ctc 96  
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
20 25 30

aag gac agg atg aac ttt gac atc cct gag gag att aag cag ctg cag 144  
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
35 40 45

cag ttc cag aag gag gac gcc gca ttg acc atc tat gag atg ctc cag 192  
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
50 55 60

aac atc ttt gct att ttc aga caa gat tca tct agc act ggc tgg aat 240  
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
65 70 75 80

gag act att gtt gag aac ctc ctg gct aat gtc tat cat cag ata aac 288  
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
85 90 95

cat ctg aag aca gtc ctg gaa gaa aaa ctg gag aaa gaa gat ttc acc 336  
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
100 105 110

agg gga aaa ctc atg agc agt ctg cac ctg aaa aga tat tat ggg agg 384

Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg	
115							120							125		
att ctg cat tac ctg aag gcc aag gag tac agt cac tgt gcc tgg acc															432	
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr	
130						135					140					
ata gtc aga gtg gaa atc cta agg aac ttt tac ttc att aac aga ctt															480	
Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu	
145						150					155			160		
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Thr	Gly	Tyr	Leu	Arg	Asn											
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			20				25					30				
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln																
			35				40				45					
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln																
			50				55				60					
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn																
			65				70				75		80			
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn																
			85				90				95					
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr																
			100				105				110					
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg																
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Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr																
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Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu																
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<220>  
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<400> 5  
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<210> 6  
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<213> Artificial Sequence

<220>  
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<210> 7  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Enterokinase recognition site oligonucleotide

<400> 7  
gacgatgatg acaag 15

<210> 8  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Enterokinase recognition site

<400> 8  
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1 5

<210> 9  
<211> 24  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Modified enterokinase
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<400> 9
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<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
      enterokinase recognition site

<400> 10
Ser Ser Gly Asp Asp Asp Asp Lys
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<210> 11
<211> 1257
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1254)

<220>
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ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc 96
Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe
    20          25          30

cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg 144
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
    35          40          45

aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc 192
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
    50          55          60

cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca 240
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala
    65          70          75          80

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ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa		288
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85	90	95
gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg		336
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu		
100	105	110
gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa		384
Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu		
115	120	125
aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg		432
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu		
130	135	140
cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag		480
His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys		
145	150	155
gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg		528
Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg		
165	170	175
aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac gtc gac		576
Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp		
180	185	190
aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga		624
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly		
195	200	205
ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc		672
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile		
210	215	220
tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtc gac cac gaa		720
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu		
225	230	235
gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat		768
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His		
245	250	255
aat gcc aag aca aag ccg ccg gag gag cag tac aac agc acg tac cgt		816
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg		
260	265	270
gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag		864
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys		
275	280	285
gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag		912
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu		
290	295	300

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac		960
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr		
305	310	315
320		
acc ctg ccc cca tcc cggtt gat gag ctg acc aag aac cag gtc agc ctg		1008
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu		
325	330	335
acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg		1056
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp		
340	345	350
gag agc aat ggg cag ccgtt gag aac aac tac aag acc acg cct ccc gtg		1104
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val		
355	360	365
ttg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac		1152
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp		
370	375	380
aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat		1200
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His		
385	390	395
400		
gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccc		1248
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro		
405	410	415
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Gly Lys		

<210> 12  
<211> 418  
<212> PRT  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
IFN-beta G162C-Ig direct fusion construct protein

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Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu  
35 40 45

Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile  
50 55 60

Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala  
65 70 75 80

Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
                   85                     90                     95  
  
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu  
                   100                    105                    110  
  
 Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu  
                   115                    120                    125  
  
 Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu  
                   130                    135                    140  
  
 His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys  
                   145                    150                    160  
  
 Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg  
                   165                    170                    175  
  
 Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp  
                   180                    185                    190  
  
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
                   195                    200                    205  
  
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
                   210                    215                    220  
  
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
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                   260                    265                    270  
  
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
                   275                    280                    285  
  
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
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 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
                   305                    310                    320  
  
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu  
                   325                    330                    335  
  
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
                   340                    345                    350  
  
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
                   355                    360                    365  
  
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
                   370                    375                    380

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
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<212> DNA

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<222> (1)..(1269)

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<223> Description of Artificial Sequence: Synthetic  
IFN-beta G162C-Ig fusion construct nucleotide sequence

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1 5 10 15

ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc 96  
Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe  
20 25 30

cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg 144  
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu  
35 40 45

aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc 192  
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile  
50 55 60

cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca 240  
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala  
65 70 75 80

ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa 288  
Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
85 90 95

gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg 336  
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu  
100 105 110

gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa 384  
Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu  
115 120 125

aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg		432	
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu			
130	135	140	
 cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag		480	
His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys			
145	150	155	160
 gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg		528	
Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg			
165	170	175	
 aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac ggc ggt		576	
Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Gly Gly			
180	185	190	
 ggc ggc agc gtc gac aaa act cac aca tgc cca ccg tgc cca gca cct		624	
Gly Gly Ser Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro			
195	200	205	
 gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag		672	
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys			
210	215	220	
 gac acc ctc atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg		720	
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val			
225	230	235	240
 gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac		768	
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp			
245	250	255	
 ggc gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac		816	
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr			
260	265	270	
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Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp			
275	280	285	
 tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc		912	
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu			
290	295	300	
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Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg			
305	310	315	320
 gaa cca cag gtg tac acc ctg ccc cca tcc ccg gat gag ctg acc aag		1008	
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys			
325	330	335	
 aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac		1056	
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp			
340	345	350	

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag		1104	
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys			
355	360	365	
acc acg cct ccc gtg ttg gac tcc gac ggc tcc ttc ttc ctc tac agc		1152	
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser			
370	375	380	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca		1200	
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser			
385	390	395	400
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc		1248	
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser			
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420			

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
IFN-beta G162C-Ig fusion construct protein

<400> 14			
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp			
1	5	10	15
Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe			
20	25	30	
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu			
35	40	45	
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile			
50	55	60	
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala			
65	70	75	80
Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln			
85	90	95	
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu			
100	105	110	
Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu			
115	120	125	
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu			
130	135	140	

His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys  
 145 150 155 160  
 Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg  
 165 170 175  
 Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Gly Gly  
 180 185 190  
 Gly Gly Ser Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 195 200 205  
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 210 215 220  
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 225 230 235 240  
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 245 250 255  
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
 260 265 270  
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 275 280 285  
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
 290 295 300  
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 305 310 315 320  
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
 325 330 335  
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 340 345 350  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 355 360 365  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 370 375 380  
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 385 390 395 400  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 405 410 415  
 Leu Ser Leu Ser Pro Gly Lys  
 420

<210> 15  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His oligonucleotide

<400> 15  
catcatcatc atcatcat 18

<210> 16  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 16  
His His His His His His  
1 5

<210> 17  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified His tag oligonucleotide

<400> 17  
tccgggggcc atcatcatca tcatacat 27

<210> 18  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Modified His tag

<400> 18  
Ser Gly Gly His His His His His His  
1 5

<210> 19  
<211> 51  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Modified His  
tag oligonucleotide

<400> 19

tccgggggcc atcatcatca tcatcatagc tccggagacg atgatgacaa g

51

<210> 20

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Modified  
His-tag

<400> 20

Ser Gly Gly His His His His His Ser Ser Gly Asp Asp Asp Asp

1

5

10

15

Lys

<210> 21

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide epitope

<400> 21

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5